

Page 1 of 8
NEMATODE PHOSPHOETHANOLAMINE N-METHYLTRANSFERASE-LIKE SEQUENCES
Deryck J. Williams et al.
12557-011001

1 gggtttaattacccaagttgagagaataaaaggtaata ATG ACC GAA GCA ATT CGA CGC TCT TCT TTC AAA AAT TTC TGG TCG
M T E A I R R S S F K N F W S
86 AAA TTT TCG CAT CGT TGT GAT AAT ACA GTA ATG ATG TTG AAT AAA AGC GCC GAT GAA TTT GAA GCC GAT GAT CGT
K F S H R C D N T V M M L N K S A D E F E A D D R
161 GCA GAT ATT ATA TCT TCA TTA CCC GAT CTA CAT GGC AAG GAT ATT GTC GAT ATT GGC GCT GGA ATT GGA CGT TTC
A D I I S S L P D L H G K D I V D I G A G I G R F
236 ACG ACA ATT TTC GCA CAT GAT GCA CGT CAT GTA CTA TCA TGC GAT TTT ATC GAA AGT TTC ATG GCA AAA AAT AAA
T T I F A H D A R H V L S C D F I E S F M A K N K
311 GAA CGG AAT GCG CAT TTC TCT AAT ATC TCT TAT CAG GTT GGC GAT GCG GTA CAT TTA CAA CTC GAT CCA AAC AGT
E R N A H F S N I S Y Q V G D A V H L Q L D P N S
386 GTA GAC CTT GTG TTC ACG AAC TGG CTC ATG ATG TAC CTC AGC GAT GAT GAA GTT ATT CGC TTT CTT CTC AAC GCA
V D L V F T N W L M M Y L S D D E V I R F L L N A
461 CTC CGA TGG CTT CGT CCT AAC GGC TAT TTG CAC CTT CGA GAG TCA TGC AGC CAA CCG TCA ACC GCA CGA GTT GGA
L R W L R P N G Y L H L R E S C S Q P S T A R V G
536 GGA ACG ATG CAT AAT AGT ACA GAG ATA AAT CCA ACC AGC TAT CGA CTA TCC TCT GAG TAT ATA AAA TTG CTA AGG
G T M H N S T E I N P T S Y R L S S E Y I K L L R
611 AAT ATT CGT TAT CGT GAA TTA GAT GGC ACA TTA TTT CGC TTC GAA GTG CAT TGG GCT TGT TCA GTG CCC ACT TAT
N I R Y R E L D G T L F R F E V H W A C S V P T Y
686 ATC GTC GTG CAA AAT AAT TGG CGT CAA GTT CAT TGG TTA ACG CAA AAA GTT CGA TGC AAC GAT GAT GCG ATA ATG
I V V Q N N W R Q V H W L T Q K V R C N D D A I M
761 TCT ATC GAA CAC CTT CTC GGA CAT TTT AGT ACA CTA TGG AAG GTG GAG CAA CAA AAG TGG GAT CGT TAC CTC GAC
S I E H L L G H F S T L W K V E Q Q K W D R Y L D
836 AAT GAA TCC TAT TGC TGG ACT GAT GAG GTG TTT GGC TAT GCG TTA ATG AAG GAA ACG ATT GAG AGT ATG CCC GCA
N E S Y C W T D E V F G Y A L M K E T I E S M P A
911 GTA TTG GCA TAT AAT CCT CGC AAA TTG GCC TAT CAT TTG CAT ATA AAT GCG CAT CGC ATT TCT GAG ATG TTA CAT
V L A Y N P R K L A Y H L H I N A H R I S E M L H
986 e TGT AAT GTT GTA TGG AAT GTG GAG ATA AAT GAA TTT TTC TAT CGG ACA TCA TTA ACG AAA GCA AAT CGC CTC AAA
C N V V W N V E I N E F F Y R T S L T K A N R L K
1061 GAT CAA CGA GTT CGA TTT GGA TGG AAT GCT ACG CTT GAA TCG TCG CTG AAT TAT TGG AAA GAA CGT GGT GCT CTC
D Q R V R F G W N A T L E S S L N Y W K E R G A L
1136 TTC GAT ATT TTT ATC GCC ACT GAA TTT TTC ACC GAT CTC GAT GAA AGT ACC ATC GAT AAG CTC TCC GTG GTA TTA
F D I F I A T E F F T D L D E S T I D K L S V V L
1211 AAA GCG GAT GCA CCT CTA ATT CTG CTG GAG CCA TTT GAC GAA TCA GCT TAT GAT GAG AAA TAC ATC ATG AAG TTG
K A D A P L I L L E P F D E S A Y D E K Y I M K L
1286 TTA TCA CGT TAT CAA CAA ATT TCT ATC GAG GAT ATC ACT GAG ATG TGC ACA GAA GCG ATT CAT AAA TAT CTA AGC
L S R Y Q Q I S I E D I T E M C T E A I H K Y L S
1361 GAA AGA GAT TTA GAG AAT AAT ATT GGA ACA AAA GTA TGG AAA TTA ATA AAA GCG CAT ATG tgattgaattttacgaaaa
E R D L E N N I G T K V W K L I K A H M
1441 aaacgacgacgacgatgattcctatgaatgttttatctgacgctgcaacgatgaatacgtattgtcataaatgagaatatgtcggct
1541 taatgcataatggcaacatataactgtgtttataaaaaaaaaaaaaaaaactacttagtcgacgcgtggccaagggcgaattctgcagatatcc
1641 atcacactggccgcgtcgagcatctagagggcccaattcgccctatagtgagtcgtattacaattcactggccgtcgatatacaacgtcgac
1741 tggaaaaaccctggcgtaaccaacttaattcgccctgcagcacat

FIGURE 1

1 gggttttaaccaggatctcaagagca ATG ACG GCT GAG GTG CGA CGG GAT TCC TTC AAG ACG TTC TGG GAC AAG TAC TCA
M T A E V R R D S F K T F W D K Y S
81 GAT AAA CCC GAC ACT AAT TCG ATG ATG CTC AAC CAG ACT GCA CAA GAT CTG GAA GCT AGC GAT AGA GCA GAT ATC
D K P D T N S M M L N Q T A Q D L E A S D R A D I
156 CTC TCC AGC CTA CCT CAC CTA ACC AAC AAA GAC GTG GTC GAT ATT GGC GCT GGA ATC GGG CGC TTC ACT ACT GTG
L S S L P H L T N K D V V D I G A G I G R F T T V
231 CTA GCA GAA ACT GCT CGA TGG GTT CTT TCA ACG GAT TTC ATC GAA TCG TTC ATC GAA AAA AAT CAA GAA CGA AAT
L A E T A R W V L S T D F I E S F I E K N Q E R N
306 GCT CAC ATG GGT AAC ATC AGT TAT CAA ATA GGA GAC GCA GTC CAT TTG CAA ATG GAC GAG AAA AGC GTG GAT CTC
A H M G N I S Y Q I G D A V H L Q M D E K S V D L
381 GTT TTT ACG AAT TGG TTG ATG ATG TAT CTC TCC GAT CGT GAA GTC ATT GAA TTT CTG CTG AAT GCT ATG CGA TGG
V F T N W L M M Y L S D R E V I E F L L N A M R W
456 TTG AGA GCG GAC GGA TAC ATT CAT CTC AGA GAA AGC TGC TCC GAG CCA AGC ACG GGC CGT CTG AAG ACC GCC ACA
L R A D G Y I H L R E S C S E P S T G R L K T A T
531 ATG CAC TCA GCC GTT GAC GCC AAC CCA ACA CAT TAC CGT TTC TCA TCG CTG TAT ATC AAG CTT CTT CGA GCA ATC
M H S A V D A N P T H Y R F S S L Y I K L L R A I
606 CGA TAC GGG GAC AGT GAT GGA AAA ATG TGG AAA TTT GAT GTG CAG TGG AGC TGC TCG GTG CCC ACC TAC ATA CGG
R Y G D S D G K M W K F D V Q W S C S V P T Y I R
681 AGG TGC AAT AAC TGG CGT CAA GTG CAT TGG TTG ACG AAG AAG GTA CCG GCA GTT GGC GAC GAA GAG ACT TCA GTC
R C N N W R Q V H W L T K K V P A V G D E E T S V
756 GAC GAT TTG CTC AAC TTG TTC AGC CAG ATC TGG CCA GCC GAA CAA AAG ACG TGG GAT GAA AAA CTA GAC AAT GAA
D D L L N L F S Q I W P A E Q K T W D E K L D N E
831 AAA TAC AGT TGG ACT GAT AAG ATA TTC TCG AAT GCG ATC GAT GAT GAA GTG GTG CCA AAG AAC AGT ACC GCC TAT
K Y S W T D K I F S N A I D D E V V P K N S T A Y
906 GTC TTC ACA CCA AGG CAA CGA TCC CCC TTC TTG CAC GTC AAC TCG CAC CTT TTG GCA GAG AAG TTC ACA TGC AAT
V F T P R Q R S P F L H V N S H L L A E K F T C N
981 GTA TGG AAT GTT GAA ACA AAA GAG TAT TTG TAT CGT ACT TCG TTG ACG AAG GCA AAC AAC CAG AAG GAC CAA CGA
V W N V E T K E Y L Y R T S L T K A N N Q K D Q R
1056 GTG CGC TTC GGT TGG AAC GAG TCC TTG TCT TCG CCC ATC GAC TAC TGG AAT CAG AGG GAC GCT TCA TTT GAC TGC
V R F G W N E S L S S P I D Y W N Q R D A S F D C
1131 ATG GTA GCA ACT GAA CTT CTC GCG ACT TGT GAT GAT GAG AGC GTA AAG AGT ATT GCG AGC ATT ATG AAA CCA GAA
M V A T E L L A T C D D E S V K S I A S I M K P E
1206 GCG AAG GTG GTG CTC CTC GAA CCA GTT AGC GGA ATT GAC GAG ACG TCC GTT AGG CAG CGA ATG ACT ACT TGT GGG
A K V V L L E P V S G I D E T S V R Q R M T T C G
1281 TTC AAA AAC ATT ACC ATC GTC GAT GTT ACA CAG GAG TCC TTG AAC GCC GAG GTT TCT TTC ATT AAG GAC CAC AAC
F K N I T I V D V T Q E S L N A E V S F I K D H N
1356 TTG GAC GTC GAA CTC TCT GGT TGT AAT TAC CTA CTG ATC AAG GCT TCA CTT taatgcaacatagaaggAACGGATGATTCT
L D V E L S G C N Y L L I K A S L
1439 ttttatacgtacttttatgaaataagccttgacattgattacggtgttgagatTTTCTGCTGCTGATCTGATGGTTGATTTACTG
1539 aagttatTTGTCCAactcattgaaattgtaaaaataacccctcaatcgaaAGAAATTGACCGGTACTTAATAAAACTTTCTCGCTAAAAAAA
1639 aaaaaaaaaaaaagtacttagtcgacgcgtggcc

FIGURE 2

1
gggttaattacccaagttgagcaattgaatat ATG CGG ATG CGA CTG GAG CAC GAG GAC ACT GAC ATG GAC TGG AGG CAA
M R M R L E H E D T D M D W R Q
83
ATT TAT CAC TCC TTT TGG AAC AAA TTT TCC GAT AGG GCT GAC AAT ACA TCC ATG CTT TTA AAT GCG GAT GCT GAT
I Y H S F W N K F S D R A D N T S M L L N A D A D
158
AAA TTT GAA GCT CTT GAC AGA GCC GAA ATT ATC GGA ATG TTG CCC TCT TTT AAA AAT AAA TTT GTT GTG GAT ATT
K F E A L D R A E I I G M L P S F K N K F V V D I
233
GGG GCG GGT ATT GGA AGA TTC ACA ACA GAA TTT GCC AAA AAG GCA AGA GAA GTG GTC TCA ACA GAT TTT GTA GCT
G A G I G R F T T E F A K K A R E V V S T D F V A
308
AGC TTT ATC GAG AAA AAT CGG GAA ACA AAT ATA GCC TTT AAT AAC ATT GAA TGG AGA GTT GGT GAT GCT GTC AGA
S F I E K N R E T N I A F N N I E W R V G D A V R
383
TTA GAT TTT GAA GAG GGG AGT ATT GAT ATA GTC TTT ACC AAT TGG CTT TTG ATG TAT TTA GTG GAT GAA GAA GTT
L D F E E G S I D I V F T N W L L M Y L V D E E V
458
GTT CAA TTT TTG ATT AAT GCC ATT AAA TGG CTC AGG CCT GGC GGT TAT TTA CAT TTG AGA GAG TCC TGC TCT GAA
V Q F L I N A I K W L R P G G Y L H L R E S C S E
533
CCT AGC AGC AAA AAA TCT AAT AAT TCG CTA CAT TCC AAT TCG GAT AGT ATC AAT CCA ACT AAA TAT CGC TTT TCA
P S S K K S N N S L H S N S D S I N P T K Y R F S
608
TCC GCA TAT ATT CAA TTG CTC AAA TCA ATT AAT TTT AAA AGC GGA GAT GGA ACC GTT TGG GGG TTT AAA ATC CAC
S A Y I Q L L K S I N F K S G D G T V W G F K I H
683
TGG GCT AGC TCT GTT AAT GTT TAT ATT CAA AAA AAT GCA AAT TGG AGA CAA GTG CAT TGG TTA GTC AGC AAG GTT
W A S S V N V Y I Q K N A N W R Q V H W L V S K V
758
CCT AAA AAG GAA AAA TTT ATG CCA AAT TTG GGT ACA CTG CTT GGA GAG AAG TGG CCT GAA GAG CAG AAG GAA TGG
P K K E K F M P N L G T L L G E K W P E E Q K E W
833
GAC AAT AAA CTT GAC TTG GCT TTG AAT GAG AAT CAG AAT ATC ACC TCA ACT CTA GCC AGT TAT CTT TTA TCT AGT
D N K L D L A L N E N Q N I T S T L A S Y L L S S
908
GGG ATT GGA ACA AAT TCA GTT ATA CTT GTT TTC GAC TTG AGA AAT AGT GAA AAT CAG CCC AGT ATT AAT GTT CAC
G I G T N S V I L V F D L R N S E N Q P S I N V H
983
ACA TTG GCT AAC AGA TTA AAT TCA AAT ATT TGG TCT GTT TCC CTC AAT CCT TTC TGC CGT CAT TCA TTA ACC
T L A N R L N S N I W S V S L N P F C F R H S L T
1058
CTT GCT AAT AAT AAC CAA GAT CGA CGG ATT AGA CAC TCT TGG CAT GAG GAT ATT GAA AGC GCT TTC CAC TTT TTG
L A N N N Q D R R I R H S W H E D I E S A F H F L
1133
GGT GAA CAA ATA TCC GGC AAA GAG AAA AAT ATC AGC AGA TTA TTT GAT GTG ATT ATT GGT ATT GGT TTG TTA GAA
G E Q I S G K E K N I S R L F D V I I G I G L L E
1208
AAA ATT AAA AAA ATG AAG GAC GCT AGC GAG AAA GTT GAG AAA ATC CTT GGC CGT TAT TTG TTA AGT ATT GAA ACA
K I K K M K D A S E K V E K I L G R Y L L S I E T
1283
GGC GAA GGA GAT GAT ATA CGA AAG GAA AAA AAG AAT GAG GAC ATT GTA GAA TAT TTC CCA TCA GAA CTA TTT ACA
G E G D D I R K E K K N E D I V E Y F P S E L F T
1358
AAA CAA ACA ATA GAA TTC AAA GCA GAT AAT GGA TTT AAT CAG CTT GAT tagaattggaaaaagagaaaaattgtgaacaaaaaa
K Q T I E F K A D N G F N Q L D
1442
aaaaaaaaaaaagtactagtcgacgcgtggcc

FIGURE 3

1 tttataaaacccagttgactaccgttttattatTTtaag ATG GAG GGT GAA AAT GAT AGA CAG AAT TTT CTT GAA TAT TGG
M E G E N D R Q N F L E Y W
84 AGA CAA TTT GGC AAT ATA GCT AAT ATC AAT GGT ATG ATG CTT AAT GCT AAT GCT TCT TTA ATT GAG AAA AAT GAT
R Q F G N I A N I N G M M L N A N A S L I E K N D
159 AGG CAT GAT GTA TGT CTA TTA CTT CCT GAT TTA AAA GGA AAA ACT GTT TTA GAT GCT GGT GCT GGA ATT GGA CGT
R H D V C L L P D L K G K T V L D A G A G I G R
234 TTT ACT GCT GAA CTT GCT GAA AGG GCT GAA AAA GTT TAT GCA TCA GAT TTT ATT TCT GAA TAT GTT ACT AAA TTA
F T A E L A E R A E K V Y A S D F I S E Y V T K L
309 CAA GAA CTT AGT GCT GAA GCG TTA AAA AAT GGA AAA ATT ATT GAT GTT ACA GTC GCA GAT GCT ACA TGT CTT TCT
Q E L S A E A L K N G K I I D V T V A D A T C L S
384 TAT CCA GAG AAT AGT TAT TTC CTT GTT TTT ACT AAT TGG TTG TTT ATG TAT TTT AAT AAT ACT GAA TGT GTA CGT
Y P E N S Y F L V F T N W L F M Y F N N T E C V R
459 TTT ACT GTA AAT GCA TTA AAA TGG TTA GAA GAA GGT GGA TAT TTT AAA TTA AGA GAA TCA TGT TCT GAA CCA TCA
F T V N A L K W L E E G G Y F K L R E S C S E P S
534 ACA AGA AGA GTT GGA AAT AGA AAT GAA ACT TCT CTT CAT GCT GCC GTT CAA TCA AAT CCA ACT GAA TAT AGA TTT
T R R V G N R N E T S L H A A V Q S N P T E Y R F
609 TCA TCT GTT TAT CTT AAA TTA ATT GAA GCA GCT AGA TAC GTT GAT TCA AAT AAT CAA AAA TGG AAA TTC GAA ATA
S S V Y L K L I E A A R Y V D S N N Q K W K F E I
684 GAA ATT TGT GGT TCT ATT CCA ACA TAC ATT TTA AAT GGT AAT ACT TGG AGA CAA GTC CAG TTA ATT GCT AAA AAA
E I C G S I P T Y I L N G N T W R Q V Q L I A K K
759 GTA AAA GCA GAT GAT AAT GAT GTT GTT TTA TCC CAA GAT GAG TTG AAA AAT TTA ATG ACT AAT GAT TGG ATA ATG
V K A D D N D V V L S Q D E L K N L M T N D W I M
834 GAA CAA AAA AAG ACT GAT TCT ATT GTT GAT GGT AGA GTC CAA TAT TTT GCT GAT AAA ATT TTT GCT AAT GAA TTA
E Q K K T D S I V D G R V Q Y F A D K I F A N E L
909 TCA AAT ATT GAT ATG ACT AAT ACT GAA TCC ATT TCA TCA ATA TTT GTT TTC CAA TCT TCA TTT AAT CCA TGG TAC
S N I D M T N T E S I S S I F V F Q S S F N P W Y
984 AAA AGA ATT TTC CCA TTT TCT TTA GCA TCA AAT AAA TAT TGC CAT GTC TGG ACA AAT GAG GGT AAT CGT GAA CTT
K R I F P F S L A S N K Y C H V W T N E G N R E L
1059 TTT AGA TGT TCA TTA ACT TCA GCT AAT GAA GAA AGA AAT ATT GGA ATG TTT TTT ACC TAT TCA AAA GAC AAT GTT
F R C S L T S A N E E R N I G M F F T Y S K D N V
1134 TTT AAT GCC TTA GAT TAC GTT AAA AAA AGA AAC TTT TTA TTA AAC AGT TTT CTA GCT ATT GAC TAT TTA AAT AAT
F N A L D Y V K K R N F L L N S F L A I D Y L N N
1209 CAT GAA GTT AAT TTT ATT GAA TCA TTT AAT AAT ATT GCT TCT CAA GAT GCT AAA ATT CTC CTT CTT GAA TCA TTT
H E V N F I E S F N N I A S Q D A K I L L E S F
1284 TCA AAT GAG GAT GAA AAA AAT TTA AAA TTA ACT AAA CTT AAT AAG CAA TAC ACA GTC AAG TGC GTC ACA GAA AAC
S N E D E K N L K L S K L N K Q Y T V K C V T E N
1359 GTT CAT AAT GAA GTT AAA AAT GTC CAT CAA GAT GAA GAA ATT GTC TGT GAC GTT ACA TCG AAA AAA TGG ATG CTT
V H N E V K N V H Q D E E I V C D V T S K K W M L
1434 ATC AAT GTC AAC CAT taatatcattcatcaagtaatgttatctaacaacgtatTTTTTattgactctaaaattcattatTTTTtaatta
I N V N H
1529 aaatattatTTacaaaaaaaatggcttaatTTTTtaataaaattaag

FIGURE 4

1 gggtttaattacccaagttgagggtggcagcgactacgcagccataaacggtag ATG CCT GCG GCA GAG CGT GAA CTA ATC AGT
M P A A E R E L I S
90 GCA TTA TTC GAC GTT ACA CCG AAA GAT GCT CTT ACA AGT GTA CTC TTG GTC ACC TCT GCC CAA TCA GAG GAA AGC
A L F D V T P K D A L T S V L L V T S A Q S E E S
165 AAT TCA TCA CTG GTT GCA CTC TTT GAG GAC AGA GCA ATT AAC GTA ACC ATC GTT GAG CGT CTT GAG GGA TTG CAA
N S S L V A L F E D R A I N V T I V E R L E G L Q
240 AGC ACT CGA GCT GAC GCA TAT GAC GCC ATT ATC AGC AAT AAA TTG ATC GTC GAG AAC TGT TTA ATC AAT AAA CCA
S T R A D A Y D A I I S N K L I V E N C L I N K P
315 TCA GAT CTC GAT ACA TTC GTC GCA TCG GCT CTA AAA GAA GAA GGT GTA CTC ATC GTT CGT GAA GAC CTA AAT GGT
S D L D T F V A S A L K E E G V L I V R E D L N G
390 TGT TCT GCG TGT GAG AAG GTC GCT CAG CTA ACG CAT TTC TTT GAT CTG TTT CGA ACA ACT CTG AAC GGC GTT ACG
C S A C E K V A Q L T H F F D L F R T T L N G V T
465 ATT GGC TTC AAA TTC TAT TCA CTC AAG CAA GTC AAT GCC TCA ATT CAT ACC GAA GGA AAC TTT CTG GAT GTC TTC
I G F K F Y S L K Q V N A S I H T E G N F L D V F
540 TGG ATA TTG CGG AAA GAA TGT TTC GAA GCG CTG GAC GAG AAC CAA AAA ACA AAA ACC TTT CGT GAT TTT CTC GAT
W I L R K E C F E A L D E N Q K T K T F R D F L D
615 690 TAT GAC GAA AAC TTA GAA GTT CTG AAG CGA TTC GGT GAT CTA AAA CCG GAT TGT AAA ATG CTC GAC ATC GGT GTT
Y D E N L E V L K R F G D L K P D C K M L D I G V
765 725 GGG ATC GGT GGA GGT GCC CGC CAG GCT AGG GAA TTC GGA GCG CTG GTT CTC GGT ATG GAT ATT AGT GCG AAT
G I G G G A R Q A A R E F G A L V L G M D I S A N
840 805 ATG CTT TCA ATA GCG ATG GAT CGC CTA CAG AAT GAG AAA GAC ACT CGC GTT CGT TAT CAA ATA TCC GAC GCT CTC
M L S I A M D R L Q N E K D T R V R Y Q I S D A L
915 900 GAA TAT GAG TTT CCA GCC AAC TCG TTT GAT TAC GTT TTC AGT CGT GAC GGT TTA CAT CAT AAC GAG CGC ATC GAC
E Y E F P A N S F D Y V F S R D G L H H N E R I D
990 965 ATC GTA ATG CGA AAG ATT TTC CAC TGG TTG AAA CCT GGT GGG AAA GTG CTC ATC ACG GTG TAT GGC ATG GGC CAT
I V M R K I F H W L K P G G K V L I T V Y G M G H
1065 1040 GGG ACA TTA AGC GCG AAA TTC CAA GCC TAT GTG GAA AAG AGG AAA TAT TTT CTG AAG ACA CTC GAA GAG ATG GTT
G T L S A K F Q A Y V E K R K Y F L K T L E E M V
1140 1115 GAG ATA ACT GAA GCT GGT GGA TTC GAA AAT GTG CAA GGG ACA AAC CTC ACC AAG CGA TTC CGC GAT ATA CTG CTC
E I T E A A G F E N V Q G T N L T K R F R D I L L
1215 1190 GAC GAG CGG ACA AAA ACG CTG AAC CGA AAA AAC GAA TTC CTT GAG AAA TTC GAT GAA GGA ACA TTC AAC AGC CTC
D E R T K T L N R K N E F L E K F D E G T F N S L
1290 1265 TTG AAC GGA TGG AAT GAT AAG ATC GGC TTT ATC GAC GAC GAT AAC CAT AAT TGG AAT CAG ATC TTC GCA ACA AAA
L N G W N D K I G F I D D D N H N W N Q I F A T K
1365 1340 CCA CTT TAG aagttccttttttgcacgggtgatcgacgtcaacagcagcgcttgaacaacactcaactatgtcttactaaatgctgcaaatt
P L *
1462 cttgcatggggcagtgctgtccgttcatcacttgaggtaaaaaactttgtaaaatatacgctt

FIGURE 5

1 gggtttaattacccaagttgagattttttcaaaaaattttaaaaataaaa ATG AGT GCA TTA TCT TGT GAA TTA GCT TAT GCA
M S A L S C E L A Y A
89
CTT CAA AAT CAT CCA AAT GCA CCC AAA AAT GGC GAA ACT GTT CTC TTA TTA ATT AAC GAT CAA GAT GTT AAT GAA
L Q N H P N A P K N G E T V L L I N D Q D V N E
164
AGG AAT TTA AAT TCT GAT CTA AGA AAT TTA TTC GAA GAT AAA TTT AAT TTG GAG GAG ATG GAT ATT GGA GAG TTG
R N L N S D L R N L F E D K F N L E E M D I G E L
239
ATA AAT ATA TCA GAA CGT TTA GAT AAA GAA GAT AAT GAC AAC GAA GAA GAG AAT TTA GAA ACA CGT TTT GAT GCT
I N I S E R L D K E D N D N E E E N L E T R F D A
314
GCT ATT TGC TCT AAT TTA TTT ATT GGA CAA GGA ATT GTA AAT GAC CGT CAT CGT ATT GCT CAA GTA TTA GGA TTA
A I C S N L F I G Q G I V N D R H R I A Q V L G L
389
CTT CTT CGT TTA ATA CGG ACA GAT GGA GTT GTA ATT ATT AGA GAA AAT CTA AAG CAA TGG GGT TCT CGT TCA ATT
L L R L I R T D G V V I I R E N L K Q W G S R S I
464
GCT GAT TTA ACT AAA TTT CTT GAT GTT TTT GCT TTT CGA AAA CAA CAA AAT AAT CAA AAA CAA CAA CAA ACA CTT
A D L T K F L D V F A F R K Q Q N N Q K Q Q Q T L
539
GGA TTT AAT TTT TAT GGA ATG AGC CAA GTA CAG GAC AGC ATT TAT GCA CAT TCT AAT TTT CTT GAC GTT TTT TGG
G F N F Y G M S Q V Q D S I Y A H S N F L D V F W
614
AGC TTA ACA ACA GCT ATT GAA GTT AGA TTA TAT GAT GAT AAA TTA GCT ACT TTT AGG GAA TTT TTG GAT AAA ACA
S L T T A I E V R L Y D D K L A T F R E F L D K T
689
CAG TAT ACT GAG GAC AAC GTT GCT AGT TAT GAG TGG ATA TTT GGG ACA GAT TTT ATC AGC CCA GGT GGA GTG AAT
Q Y T E D N V A S Y E W I F G T D F I S P G G V N
764
GAA AAT AGA AGA GTA CTA AAA TAT TTC CGT CAT TTA CGT CCA GGA CAA CAA ATG CTT GAT ATT GGT GTT GGA ATT
E N R R V L K Y F R H L R P G Q Q M L D I G V G I
839
GGT GGA GGA GCT AGA CAA GCT GCT AGG GAG TTT GGT CTT CAA GTA CTT GGT TGT GAT CTT TCT TCA AAT ATG ATT
G G G A R Q A A R E F G L Q V L G C D L S S N M I
914
CAA CAT GCT TTT GAT CGT AAT CAA CGT GAC AAA GAT CAT CGT GTT GAA TAT CAA ATT GCT GAT GCT ATG GTT TAT
Q H A F D R N Q R D K D H R V E Y Q I A D A M V Y
989
CGT TAT GAA TCT AAT GCT TTT GAT ATT GTA TTT AGT AGA GAT TGT ATT CAA CAT ATT AAA GAT ACA AAA AGA TTA
R Y E S N A F D I V F S R D C I Q H I K D T K R L
1064
TTT AGA AAT ATT TAT ACT TGG CTT AAA CCA GGT GGA CAA GTA CTT GTT ACA ATG TAT GGG AAA GGA CAT GGA GTT
F R N I Y T W L K P G G Q V L V T M Y G K G H G V
1139
CTC TCG CCA AAA TTT CAT GAA TAT GTT CGT AAA CGG CAA TAT GCA CTA AAA ACT TTA GAA GAA TAT AGA GAA ATT
L S P K F H E Y V R K R Q Y A L K T L E E Y R E I
1214
GCT CAT AAT GTT GGT TTA ACA ACT ATT TAC ACA GAA AAT ATG ACT AAA CGT TTG AGA GAA ATT TTA GTA ATT GAA
A H N V G L T T I Y T E N M T K R L R E I L V I E
1289
CGT GAT AGA GCA GTT GAA AAT AAA GAA GAA TTT ATT CAA AAA TTT AGT GAA AAA CTT TAT TCA AAA TTA ATT GAG
R D R A V E N K E E F I Q K F S E K L Y S K L I E
1364
GGT TGG GCA GAT AAA TTA CAA TTT ATT GAT GAA GAT AAC CAA AAT TGG TTG TTA CTT CGT GCG GAG AAA CCG GTG
G W A D K L Q F I D E D N Q N W L L R A E K P V
1439
CAT CCG CAT GCT TAT TTA ACT GAA GCT GGA GCT taaaacaaattatTTaaagacaagaaaataaagagaagaaaatttttaattttt
H P H A Y L T E A G A
1528
tatataca

FIGURE 6

C_elegans_a	...MSTDQ9.....SSVEDQTVAMVNVRANFKSFWDKYSKPDTSNSMMLNHSAAELES:	51
C_elegans_b	MDRYSPYDKTVLIFCTAYILOKAMVNVRANFKSFWDKYSKPDTSNSMMLNHSAAELES:	60
H_contortusMTAEVRRDSFKTFWDKYSKPDTSNSMMLNQTAQDLEA:	37
A_summMTEAIRSSFKNFWSKFSHRCNTVMMLNKSADFEA:	37
M_incognitaMRMRLEHEDTMDWRQIYHSFWNKFSRADNTSMLLNADAKFEA:	45
S_stercoralisMEGENDRQNFFLEYWRQFGNIANINGMMLNANASLIEK:	37
C_elegans_a	SDRADILASLPPLLHNKDVVDIGAGIGRFTTVLAETARWVLSTDFIDSFIKKNQERNNAHLG:	111
C_elegans_b	SDRADILASLPPLLHNKDVVDIGAGIGRFTTVLAETARWVLSTDFIDSFIKKNQERNNAHLG:	120
H_contortus	SDRADILSSLPHLTNKDVVDIGAGIGRFTTVLAETARWVLSTDFIESFIEKNQERNNAHMG:	97
A_summ	DDRADIISSLPDLHGKDIVDIGAGIGRFTTIFAHDARHVLSCDFIESFMAKNKERNNAFS:	97
M_incognita	LDRAEIIGMLPSFKNKVVUDIGAGIGRFTTEFAKKAREVVSTDFVASFIEKNRETNIAFN:	105
S_stercoralis	NDRHDVCLLPDLKGKTVLDAGAGIGRFTAELAERAEVYASDFISEYVTKLQELSAAEAL:	97
C_elegans_a	N....INYQVGDAVGLKMECSVLDLVFTNWLMYLSDEETVEFIFNCMRWLRSHGIVHLR:	167
C_elegans_b	N....INYQVGDAVGLKMECSVLDLVFTNWLMYLSDEETVEFIFNCMRWLRSHGIVHLR:	176
H_contortus	N....ISYQIGDAVHLQMDEKSVDLVFTNWLMYLSREVIEFLNNAMRWLRADGYIHHLR:	153
A_summ	N....ISYQVGDAVHLQLDPNSVLDVFTNWLMYLSDEVIRFLNLARWLRPNGYLHLR:	153
M_incognita	N....IEWRVGDAVRLDFFEEGSIDIVFTNWLMYLVDEEVVQFLINAIRWLRPGGYLHLR:	161
S_stercoralis	KNGKIIDVTVAADATCLSYPPNSYFLVFTNWLFMFYFNNTECVRFTVNALKWLEEGGYFKLR:	157
C_elegans_a	ESCSEPSTGRS...KAKSMHDTANANPHTYRFSSLYINLLRAIRYRDVDNKLWRFNVQWS:	224
C_elegans_b	ESCSEPSTGRS...KAKSMHDTANANPHTYRFSSLYINLLRAIRYRDVDNKLWRFNVQWS:	233
H_contortus	ESCSEPSTGRL...KTATMHSAVDANPHTYRFSSLYIKLLRAIRYGDSDGKMWKFDVQWS:	210
A_summ	ESCSEPSTAR...VGGTMHNSTEINPTSYRLSSEYIKLLRNIRYRELDGTLFRFEVHWA:	209
M_incognita	ESCSEPSSKK...NNSLHSNSDSINPTKYRFSSAYIQLLKSINFSGDGTWCGFKIHWA:	218
S_stercoralis	ESCSEPSTRRVGNRNETSLHAAVQSNPTEYRFSSVYLKLIEARRYVDSDNNQWKFEIEIC:	217
C_elegans_a	CSVPTYIKRSNNWRQVHWLAEKVPaedGAKGTSFNLVELIKNTWQNEQEAWDAKLD...:	281
C_elegans_b	CSVPTYIKRSNNWRQVHWLAEKVPaedGAKGTSFNLVELIKNTWQNEQEAWDAKLD...:	290
H_contortus	CSVPTYIIRRCCNNWRQVHWLTKKVPAVGDEE.TSVDDLLNFSQIWPRAEQKWTWDEKLD...:	266
A_summ	CSVPTYIIVVQNNWRQVHWLTKVRCNDAAI.MSIEHLLGHFSTLWKVEQQWKDRYLD...:	265
M_incognita	SSVNVYIQLKNAWRQVHWLVSKVPKKE...KMPNLGTLLGEKWPSEEQKEWDNKLDLAL:	274
S_stercoralis	GSIPTYIILNGNTWRQVQLIAKKVKADDNDVVLSQLDELKNLMTNDWIMEQKKTDSIVD...:	274
C_elegans_a	DEKYVWTDKVFSSALT....SLPSNSTFFLYTPRTVSPYCHINAHTLAETFNNAN.VWNT:	335
C_elegans_b	DEKYVWTDKVFSSALT....SLPSNSTFFLYTPRTVSPYCHINAHTLAETFNNAN.VWNT:	344
H_contortus	NEKYSWTDKIFNSNAIDDE...VVPKNSTAYVFTPQRSPFLHVNSHLLAEKFTCN.VWNV:	322
A_summ	NESYCWTDKIFNSNAIDDE...TIESMPAVLAYNPRLAYHLHINAHRISEMLHCNVVWNV:	322
M_incognita	NENQNITSTLASYLLSS...GIGTNSVILVFDLRNSENQPSINVHTLANRLNSN.IWSV:	329
S_stercoralis	GRVQYFADKIFANELSNIDMTNTESISSIFVFQSSFNPWYKRIFPPSLASNKYCH.VWTN:	333
C_elegans_a	EIIPEYYRTSLTKSNNLKDQRVRFGWN.QSLTDSVTWQOKDALFDVFVATEFLSTVDDE:	394
C_elegans_b	EIIPEYYRTSLTKSNNLKDQRVRFGWN.QSLTDSVTWQOKDALFDVFVATEFLSTVDDE:	403
H_contortus	ETKEYLYRTSLTKANNQKDQRVRFGWN.ESSLSSPIDYWNQRDASFDCMVATELLATCDE:	381
A_summ	EINEFFYRTSLTKANRLKDQRVRFGWN.ATLESSLNWKERGALFDIFIATEEFFTDLDES:	381
M_incognita	SLNPFCFRHSLTLANNQDRRIRHSHW.EDIESAFHFLGEQISGKEKNISRLFVIIGIG:	388
S_stercoralis	EGNRELFRCSLTSANEERNIGMFTTYSKDNVFNALDYVKKRNFLNSFLAIDYLNHEVN:	393
C_elegans_a	TIRQLPNVMSDGAKFITLEP..VDEVNEAEMKQRIQELGYTLKSFTDVTDOCIEAQEQYF:	452
C_elegans_b	TIRQLPNVMSDGAKFITLEP..VDEVNEAEMKQRIQELGYTLKSFTDVTDOCIEAQEQYF:	461
H_contortus	SVKSIASIMKPEAKVVLLEP..VSGIDETSVRQRMTCGFKNITIVDVTQESLNAEVFSI:	439
A_summ	TIDKLSVVLKADAPLILEP..FDESAYDEKYIMKLLSRYQQISIEDITEMCTEAIHKYL:	439
M_incognita	LLEKIKKMKDASEKVEKILGRYLLSIETGEGDDIRKEKKNEDIVEYFPSELFTKQTIEFK:	448
S_stercoralis	FIESFNNIASQDAKILLES..FSNEDE...KNLKLSKLNQYTVKCVTENVHNEVKNVH:	448
C_elegans_a	KDHEQLRDEKVIRKNWVLLELTH:475	
C_elegans_b	KDHEQLRDEKVIRKNWVLLELTH:484	
H_contortus	KDHN..LDVELSGCNYLLLIKASL:460	
A_summ	SERD..LENNIGTKVWKLIKHAM:460	
M_incognita	ADNG.....FNQLD...:457	
S_stercoralis	QDEE..IVCDVTSKKWMLINVNH:469	

FIGURE 7

A_suum MP..AAERELISALFDVTPKDALTSLVLLVTSAQSEES..NSSLVALFEDRA.....I: 48
C_elegans MSSLSIPRQS LYVNVKTEGRSVSNVQVVSPCQKQ....GQTYVTAFTPLT.....S: 48
M_javanica MSALSCELAYALQNHPNAPKNGETVLLLINDQDVNERNLNSDLRNLFEDKFNLLEMDIGE: 60

A_suum NVTIVERLEGLQSTRA.....DAYDAIISNKLIVENCLIN..KPSDLDTFVASALKEEG:100
C_elegans NVQVHTSLEQLSTIR.....NADVLIFNNALSQIITNAD..LLTDFLKNATNATAIGG: 99
M_javanica LINISERLDKEDNDNEEENLETFRDAICSNLFIGQGIVNDRHRIAQVLGLLLRLIRTDG:120

A_suum VLIVREDLNGCSACEKVAQLTHFFDLFRRTT.LNGV.....TIGFKFYSLKQVNASIHTEG:154
C_elegans TVIIREDLKDCSDKRQVARLTDYFDVFRRTDSDGN.....NTGLDLYTVQVEHSNYVEQ:154
M_javanica VVIIRENLKQWGS.RSIADLTFLDVFAFRKQQNNQKQQQLGFNFYGMSSQVQDSIYAH:179

A_suum NFLDVFWILRKECFEALDENQKTKTFRDFLDTTQYTDESIRAYEWIFGDNFISP GGYDEN:214
C_elegans NFLDFIFVFRKKVFAPTTD..ATITFRDFLDKTQYTNTGIDAYEWMFGVNFISP GGYDEN:212
M_javanica NFLDVFWSLTTAIEVRLYDD.KLATFREFLDTQYTEDNVASYEWIFGTDFISP GGVNEN:238

A_suum LEVLKRGFDLKPDCKMLDIGVGIGGGARQAAREFGALVLGMDISANMLS IAMDRLQNEKD:274
C_elegans LKIIKRGDFKPGQTMLDIGVGIGGGARQVADEFGVHVHGIDLSSNMLAIALERLHEEKD:272
M_javanica RRVLKYFRHLRPGQQMLDIGVGIGGGARQAAREFGLQVLGCDLSSNMIQHAFDRNQRDKD:298

A_suum TRVRYQISDALEYEFPANSFDYVFSRDGLHHNERIDIVMRKIFHWLKPGGVLI TVYGMG:334
C_elegans SRVKYSITDALVYQFEDNSFDYVFSRDCIQHHIPDTEKLF SRIYKALKPGGVLI TVMYGKG:332
M_javanica HRVEYQIADAMVYRYESNAFDIVFSRDCIQHIKDTKRLFRNIYTWLKPGQVLT MYGKG:358

A_suum HGTL SAKFQAYVEKRKYFLKTLEEMVEITEAAGFENVQGTNLTKRFDILL DERTKTLNR:394
C_elegans YGEQSDKFKTYVAQRAYFLKLNKEIADIANKTGFVNQVTENMTPRFKEILLEERGHLEQN:392
M_javanica HGVLSPKFHEYVRKRQYALKTLEEYREIAHNVGLTTIYTENMTKRLREILVIERDRAVEN:418

A_suum KNEFLEKFDEGTFNSSLNGWN DKIGFIDDDNNWNQIFATKPL.....:437
C_elegans EAEFMSKFTQRERDSLISGWTDKLGYIEKDHNWNFFLAQKPFPK.....:437
M_javanica KEEFIQKFSEKLYSKLIEGWADKLQFIDE DNQNWL RAEKPVPHAYLTEAGA:472

FIGURE 8